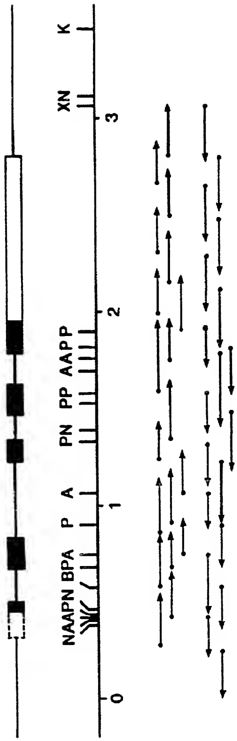

FIG.1

FIG. 2A

```
                          HindIII
5' - AGCTTGGACTCAGCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG[fNNNNN]

                -12     -10                                  -1  +1
                Leu Trp His Ser Ala Leu Trp Thr Val Gln Glu Ala Thr Pro Leu Gly Pro
                CTG TGG CAC AGT GCA CTC TGG ACA GTG CAG GAA GCC ACC CCC CTG GGC CCT
                GAC ACC GTG TCA CGT GAG ACC TGT CAC GTC CTT CGG TGG GGG GAC CCG GGA
                            HgiAI                                           ApaI
                    10                                  20
Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu Lys Cys Leu Glu Gln Val Arg Lys Ile Gln
GCC AGC TCC CTG CCC CAG AGC TTC CTG CTC AAG TGC TTA GAG CAA GTG AGG AAG ATC CAG
CGG TCG AGG GAC GGG GTC TCG AAG GAC GAG TTC ACG AAT CTC GTT CAC TCC TTC TAG GTC

                    30                                  40
Gly Asp Gly Ala Ala Leu Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu
GGC GAT GGC GCA GCG CTC CAG GAG AAG CTG TGT GCC ACC TAC AAG CTG TGC CAC CCC GAG
CCG CTA CCG CGT CGC GAG GTC CTC TTC GAC ACA CGG TGG ATG TTC GAC ACG GTG GGG CTC

                    50                                  60
Glu Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser Cys Pro
GAG CTG GTG CTG CTC GGA CAC TCT CTG GGC ATC CCC TGG GCT CCC CTG AGC AGC TGC CCC
CTC GAC CAC GAC GAG CCT GTG AGA GAC CCG TAG GGG ACC CGA GGG GAC TCG TCG ACG GGG

                    70                                  80
Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His Ser Gly Leu Phe Leu Tyr
AGC CAG GCC CTG CAG CTG GCA GGC TGC TTG AGC CAA CTC CAT AGC GGC CTT TTC CTC TAC
TCG GTC CGG GAC GTC GAC CGT CCG ACG AAC TCG GTT GAG GTA TCG CCG GAA AAG GAG ATG

                    90                                  100
Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr
CAG GGG CTC CTG CAG GCC CTG GAA GGG ATC TCC CCC GAG TTG GGT CCC ACC TTG GAC ACA
GTC CCC GAG GAC GTC CGG GAC CTT CCC TAG AGG GGG CTC AAC CCA GGG TGG AAC CTG TGT
```

FIG. 2B

```
                110                                     120
Leu Gln Leu Asp Val Ala Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly
CTG CAG CTG GAC GTC GCC GAC TTT GCC ACC ACC ATC TGG CAG CAG ATG GAA GAA CTG GGA
GAC GTC GAC CTG CAG CGG CTG AAA CGG TGG TGG TAG ACC GTC GTG TAC CTT CTT GAC CCT

                130                                     140
Met Ala Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe Gln
ATG GCC CCT GCC CTG CAG CCC ACC CAG GGT GCC ATG CCG GCC TTC GCC TCT GCT TTC CAG
TAC CGG GGA CGG GAC GTC GGG TGG CTC CCA CGG TAC GGC CGG AAG CGG AGA CGA AAG GTC

                150                                     160
Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser Phe Leu Glu Val Ser Tyr
CGC CGG GCA GGA GGG GTC CTG GTT GCC TCC CAT CTG CAG AGC TTC CTG GAG GTG TCG TAC
GCG GCC CGT CCT CCC CAG GAC CAA CGG AGG GTA GAC GTC TCG AAG GAC CTC CAC AGC ATG

                170             174
Arg Val Leu Arg His Leu Ala Gln Pro OP
CGC GTT CTA CGC CAC CTT GCC CAG CCC TGA GCC AAG CCC TCC CCA TCC CAT GTA TTT ATC
CGC CAA GAT GCG GTG GAA CGG GTC GGG ACT

TCT ATT TAA TAT TTA TGT CTA TTT AAG CCT CAT ATT TAA AGA CAG GGA AGA GCA GAA CGG

AGC CCC AGG CCT CTG TGT CCT TCC CTG CAT TTC TGA GTT TCA TTC TCC TGC CTG TAG CAG
        StuI

TGA GAA AAA GCT CCT GTC CTC CCA TCC CCT GGA CTG GGA GGT AGA TAG GTA AAT ACC AAG

TAT TTA TTA CTA TGA CTG CTC CCC AGC CCT GGC TCT GCA ATG GGC ACT GGG ATG AGC CGC

TGT GAG CCC CTG GTC CTG AGG GTC CCC ACC TGG GAC CCT TGA GAG TAT CAG GTC TCC CAC
```

FIG. 2C

GTG GGA GAC AAG AAA TCC CTG TTT AAT ATT TAA ACA GCA GTG TTC CCC ATC TGG GTC CTT

GCA CCC CTC ACT CTG GCC TCA GCC GAC TGC ACA GCG GCC CCT GCA TCC CCT TGG CTG TGA

GGC CCC TGG ACA AGC AGA GGT GGC CAG AGC TGG GAG GCA TGG CCC TGG GGT CCC ACG AAT

TTG CTG GGG AAT CTC GTT TTT CTT CTT AAG ACT TTT GGG ACA TGG TTT GAC TCC CGA ACA

TCA CCG ACG TGT CTC CTG TTT TTC TGG GTG GCC TCG GGA CAC CTG CCC TGC CCC CAC GAG

GGT CAG GAC TGT GAC TCT TTT TAG GGC CAG GCA GGT GCC TGG ACA TTT GCC TTG CTG GAC

GGG GAC TGG GGA TGT GGG AGG GAG CAG ACA GGA GGA ATC ATG TCA GGC CTG TGT GTG AAA
StuI

GGA AGC TCC ACT GTC ACC CTC CAC CTC TTC ACC CCC CAC TCA CCA GTG TCC CCT CCA CTG

TCA CAT TGT AAC TGA ACT TCA GGA TAA TAA AGT GTT TGC CTC CA

[f150-200 base poly A plus 25-30 bases plasmid DNA preceding a PvuII restriction site]-3'

```
GGGGACAGGCTTGAGAATCCCAAAGGAGAGGGGCAAAGGACACTGCCCCCGCAAGTCTGCCAGAGCAGAG    70

AGGGAGACCCCGACTCAGCTGCCACTTCCCCACAGGCTCGTGCCGCTTCCAGGCGTCTATCAGCGGCTCA   140

GCCTTTGTTCAGCTGTTCTGTTCAAACACTCTGGGGCCATTCAGGCCTGGGTGGGGCAGCGGGAGGAAGG   210

GAGTTTGAGGGGGGCAAGGCGACGTCAAAGGAGGATCAGAGATTCCACAATTTCACAAAACTTTCGCAAA   280

CAGCTTTTTGTTCCAACCCCCCTGCATTGTCTTGGACACCAAATTTGCATAAATCCTGGGAAGTTATTAC   350

TAAGCCTTAGTCGTGGCCCCAGGTAATTTCCTCCCAGGCCTCCATGGGGTTATGTATAAAGGGCCCCCTA   420
                                                                -30
                                                   MetAlaGlyProAlaThr
GAGCTGGGCCCCAAAACAGCCCGGAGCCTGCAGCCCAGCCCCACCCAGACCCATGGCTGGACCTGCCACC   490
          -20   -18
GlnSerProMetLysLeuMetA
CAGAGCCCCATGAAGCTGATGGGTGAGTGTCTTGGCCCAGGATGGAGAGCCGCCTGCCCTGGCATGGGA   560

GGGAGGCTGGTGTGACAGAGGGGCTGGGGATCCCCGTTCTGGGAATGGGGATTAAAGGCACCCAGTGTCC   630
                                                                   -16
                                                        laLeuGlnLeuL
CCGAGAGGGCCTCAGGTGGTAGGGAACAGCATGTCTCCTGAGCCCGCTCTGTCCCCAGCCCTGCAGCTGC   700
```

FIG. 3A

```
  -10                                -1 +1                                    10
euLeuTrpHisSerAlaLeuTrpThrValGlnGluAlaThrProLeuGlyProAlaSerSerLeuProGl
TGCTGTGGCACAGTGCACTCTGGACAGTGCAGGAAGCCACCCCCCTGGGCCCTGCCAGCTCCCTGCCCCA    770
                   20                                  30
nSerPheLeuLeuLysCysLeuGluGlnValArgLysIleGlnGlyAspGlyAlaAlaLeuGlnGluLys
GAGCTTCCTGCTCAAGTGCTTAGAGCAAGTGAGGAAGATCCAGGGCGATGGCGCAGCGCTCCAGGAGAAG    840
 35
Leu
CTGGTGAGTGAGGTGGGTGAGAGGGCTGTGGAGGGAAGCCCGGTGGGGAGAGCTAAGGGGGATGGAACTG    910

CAGGGCCAACATCCTCTGGAAGGGACATGGGAGAATATTAGGAGCAGTGGAGCTGGGGAAGGCTGGGAAG    980

GGACTTGGGGAGGAGGACCTTGGTGGGGACAGTGCTCGGGAGGGCTGGCTGGGATGGGAGTGGAGGCATC    1050

ACATTCAGGAGAAAGGGCAAGGGCCCCTGTGAGATCAGAGAGTGGGGGTGCAGGGCAGAGAGGAACTGAA    1120

CAGCCTGGCAGGACATGGAGGGAGGGGAAAGACCAGAGAGTCGGGGAGGACCCGGGAAGGAGCGGCGACC    1190
                                                36         40
                                               CysAlaThrTyrLysLeuCysHisProGlu
CGGCCACGGCGAGTCTCACTCAGCATCCTTCCATCCCCAGTGTGCCACCTACAAGCTGTGCCACCCCGAG    1260
             50                                60
GluLeuValLeuLeuGlyHisSerLeuGlyIleProTrpAlaProLeuSerSerCysProSerGlnAlaL
GAGCTGGTGCTGCTCGGACACTCTCTGGGCATCCCCTGGGCTCCCCTGAGCAGCTGCCCCAGCCAGGCCC    1330
```

FIG. 3B

```
   70  71
euGlnLeu
TGCAGCTGGTGAGTGTCAGGAAAGGATAAGGCTAATGAGGAGGGGAAGGAGAGGAGGAACACCCATGGG    1400

CTCCCCCATGTCTCCAGGTTCCAAGCTGGGGGCCTGACGTATCTCAGGCAGCACCCCCTAACTCTTCCGC    1470
           72                   80                             90
           AlaGlyCysLeuSerGlnLeuHisSerGlyLeuPheLeuTyrGlnGlyLeuLeuGlnA
TCTGTCTCACAGGCAGGCTGCTTGAGCCAACTCCATAGCGGCCTTTTCCTCTACCAGGGGCTCCTGCAGG    1540

                        100                          110
laLeuGluGlyIleSerProGluLeuGlyProThrLeuAspThrLeuGlnLeuAspValAlaAspPheAl
CCCTGGAAGGGATCTCCCCCGAGTTGGGTCCCACCTTGGACACACTGCAGCTGGACGTCGCCGACTTTGC    1610
               120
aThrThrIleTrpGlnGln
CACCACCATCTGGCAGCAGGTGAGCCTTGTTGGGCAGGGTGGCCAAGGTCGTGCTGGCATTCTGGGCACC    1680

ACAGCCGGGCCTGTGTATGGGCCCTGTCCATGCTGTCAGCCCCCAGCATTTCCTCATTTGTAATAACGCC    1750
                                                  121
                                                  MetGluGluLeuGlyMetAlaProAla
CACTCAGAAGGGCCCAACCACTGATCACAGCTTTCCCCCACAGATGGAAGAACTGGGAATGGCCCCTGCC    1820
    130                       140                           150
LeuGlnProThrGlnGlyAlaMetProAlaPheAlaSerAlaPheGlnArgArgAlaGlyGlyValLeuV
CTGCAGCCCACCCAGGGTGCCATGCCGGCCTTCGCCTCTGCTTTCCAGCGCCGGGCAGGAGGGGTCCTGG    1890
```

FIG. 3C

```
                     160                                170      174
alAlaSerHisLeuGlnSerPheLeuGluValSerTyrArgValLeuArgHisLeuAlaGlnProOP
TTGCCTCCCATCTGCAGAGCTTCCTGGAGGTGTCGTACCGCGTTCTACGCCACCTTGCCCAGCCCTGAGC   1960

CAAGCCCTCCCCATCCCATGTATTTATCTCTATTTAATATTTATGTCTATTTAAGCCTCATATTTAAAGA   2030

CAGGGAAGAGCAGAACGGAGCCCCAGGCCTCTGTGTCCTTCCCTGCATTTCTGAGTTTCATTCTCCTGCC   2100

TGTAGCAGTGAGAAAAAGCTCCTGTCCTCCCATCCCCTGGACTGGGAGGTAGATAGGTAAATACCAAGTA   2170

TTTATTACTATGACTGCTCCCCAGCCCTGGCTCTGCAATGGGCACTGGGATGAGCCGCTGTGAGCCCCTG   2240

GTCCTGAGGGTCCCCACCTGGGACCCTTGAGAGTATCAGGTCTCCCACGTGGGAGACAAGAAATCCCTGT   2310

TTAATATTTAAACAGCAGTGTTCCCCATCTGGGTCCTTGCACCCCTCACTCTGGCCTCAGCCGACTGCAC   2380

AGCGGCCCCTGCATCCCCTTGGCTGTGAGGCCCCTGGACAAGCAGAGGTGGCCAGAGCTGGGAGGCATGG   2450

CCCTGGGGTCCCACGAATTTGCTGGGGAATCTCGTTTTTCTTCTTAAGACTTTTGGGACATGGTTTGACT   2520

CCCGAACATCACCGACGTGTCTCCTGTTTTTCTGGGTGGCCTCGGGACACCTGCCCTGCCCCCACGAGGG   2590
```

FIG. 3D

TCAGGACTGTGACTCTTTTTAGGGCCAGGCAGGTGCCTGGACATTTGCCTTGCTGGATGGGGACTGGGGA 2660

TGTGGGAGGGAGCAGACAGGAGGAATCATGTCAGGCCTGTGTGTGAAAGGAAGCTCCACTGTCACCCTCC 2730

ACCTCTTCACCCCCCACTCACCAGTGTCCCCTCCACTGTCACATTGTAACTGAACTTCAGGATAATAAAG 2800

TGTTTGCCTCCAGTCACGTCCTTCCTCCTTCTTGAGTCCAGCTGGTGCCTGGCCAGGGGCTGGGGAGGTG 2870

GCTGAAGGGTGGGAGAGGCCAGAGGGAGGTCGGGGAGGAGGTCTGGGGAGGAGGTCCAGGGAGGAGGAGG 2940

AAAGTTCTCAAGTTCGTCTGACATTCATTCCGTTAGCACATATTTATCTGAGCACCTACTCTGTGCAGAC 3010

GCTGGGCTAAGTGCTGGGGACACAGCAGGGAACAAGGCAGACATGGAATCTGCACTCGAG 3070

FIG. 3E

FIG. 4

```
EChpG-CSFDNA SECTION I

        10   1      20         30         40   2      50         60
 CTAGAAAAA ACCAAGGAGG TAATAAATAA TGACTCCATT AGGTCCTGCT TCTTCTCTGC
     TTTTT TGGTTCCTCC ATTATTTATT ACTGAGGTAA TCCAGGACGA AGAAGAGACG
              8                                   9
  XbaI

        70    3     80         90        100    4  110        120
CGCAAAGCTT TCTGCTGAAA TGTCTGGAAC AGGTTCGTAA AATCCAGGGT GACGGTGCTG
GCGTTTCGAA AGACGACTTT ACAGACCTTG TCCAAGCATT TTAGGTCCCA CTGCCACGAC
             10                                  11

       130  5      140        150        160   6   170        180
CACTGCAAGA AAAACTGTGC GCTACTTACA AACTGTGCCA TCCGGAAGAG CTGGTACTGC
GTGACGTTCT TTTTGACACG CGATGAATGT TTGACACGGT AGGCCTTCTG GACCATGACG
            12                                  13

   7   190        100
TGGGTCATTC TCTTGG
ACCCAGTAAG AGAACCCTAG
    14
                BamHI
```

FIG. 5

ECHpG-CSFDNA SECTION II

```
       10     15   20         30         40   16     50         60
 GATCCCGTG GGCTCCGCTG TCTTCTTGTC CATCTCAAGC TCTTCAGCTG GCTGGTTGTC
     GGCAC CCGAGGCGAC AGAAGAACAG GTAGAGTTCG AGAAGTCGAC CGACCAACAG
              23                                 24
BamHI

        70 17       80         90    18 100        110    19 120
TGTCTCAACT GCATTCTGGT CTGTTCCTGT ATCAGGGTCT TCTGCAAGCT CTGGAAGGTA
ACAGAGTTGA CGTAAGACCA GACAAGGACA TAGTCCCAGA AGACGTTCGA GACCTTCCAT
            25                      26                     27

       130        140   20    150        160        170   21    180
TCTCTCCGGA ACTGGGTCCG ACTCTGGACA CTCTGCAGCT AGATGTAGCT GACTTTGCTA
AGAGAGGCCT TGACCCAGGC TGAGACCTGT GAGACGTCGA TCTACATCGA CTGAAACGAT
                         28                              29

       190        200  22     210
CTACTATTTG GCAACAGATG GAAGAGCTCA AAG
GATGATAAAC CGTTGTCTAC CTTCTCGAGT TTCTTAA
                       30
                          SstI          EcoRI
```

FIG. 6

EChpG-CSFDNA SECTION III

```
        10       31  20         30         40    32    50         60
 GATCCAAAG AGCTCGGTAT GGCACCAGCT CTGCAACCGA CTCAAGGTGC TATGCCGGCA
     GTTTC TCGAGCCATA CCGTGGTCGA GACGTTGGCT GAGTTCCACG ATACGGCCGT
                  37                                  38
BamHI      SstI

        70    33    80         90        100    34 110        120
TTCGCTTCTG CATTCCAGCG TCGTGCAGGA GGTGTACTGG TTGCTTCTCA TCTGCAATCT
AAGCGAAGAC GTAAGGTCGC AGCACGTCCT CCACATGACC AACGAAGAGT AGACGTTAGA
               39                                  40

   35  130        140        150    36  160        170
TTCCTGGAAC TATCTTACCG TGTTCTGCGT CATCTGGCTC AGCCGTAATA G
AAGGACCTTC ATAGAATGGC ACAAGACGCA GTAGACCGAG TCGGCATTAT CTTAA
     41                                    42
                                                          EcoRI
```

FIG. 7A

```
                                          -1  +1
                                         Met Thr Pro Leu Gly Pro Ala Ser Ser Leu
  C TAG AAA AAA CCA AGG AGG TAA TAA ATA ATG ACT CCA TTA GGT CCT GCT TCT TCT CTG

 10                                      20
CCG CAA AGC TTT CTG CTG AAA TGT CTG GAA CAG GTT CGT AAA ATC CAG GGT GAC GGT GCT
Pro Gln Ser Phe Leu Leu Lys Cys Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala

 30                                      40
Ala Leu Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu Val Leu
GCA CTG CAA GAA AAA CTG TGC GCT ACT TAC AAA CTG TGC CAT CCG GAA GAG CTG GTA CTG

 50                                      60
Leu Gly His Ser Leu Gly Ile Pro Trp ala Pro Leu Ser Ser Cys Pro Ser Gln Ala Leu
CTG GGT CAT TCT CTT GGG ATC CCG TGG GCT CCG CTG TCT TCT TGT CCA TCT CAA GCT CTT

 70                                      80
Gln Leu Ala Gly Cys Leu Ser Gln leu His Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu
CAG CTG GCT GGT TGT CTG TCT CAA CTG CAT TCT GGT CTG TTC CTG TAT CAG GGT CTT CTG

 90                                      100
Gln Ala Leu Glu Gly Ile Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp
CAA GCT CTG GAA GGT ATC TCT CCG GAA CTG GGT CCG ACT CTG GAC ACT CTG CAG CTA GAT

110                                      120
Val Ala Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu leu Gly Met Ala Pro Ala
GTA GCT GAC TTT GCT ACT ACT ATT TGG CAA CAG ATG GAA GAG CTC GGT ATG GCA CCA GCT

130                                      140
Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe Gln Arg Arg Ala Gly
CTG CAA CCG ACT CAA GGT GCT ATG CCG GCA TTC GCT TCT GCA TTC CAG CGT CGT GCA GGA
```

FIG. 7B

```
150                                     160
Gly Val Leu Val Ala Ser His Leu Gln Ser Phe Leu Glu Val Ser Tyr Arg Val Leu Arg
GGT GTA CTG GTT GCT TCT CAT CTG CAA TCT TTC CTG GAA GTA TCT TAC CGT GTT CTG CGT

170             174
His Leu Ala Gln Pro
CAT CTG GCT CAG CCG TAA TAG AAT T
```

FIG. 8

```
1   ATCGATTTGATTCTAGAAGGAGGAATAACATATGGTTAACGCGTTGGAATTCGGTACCAT
    TAGCTAAACTAAGATCTTCCTCCTTATTGTATACCAATTGCGCAACCTTAAGCCATGGTA

    1 Clal, 12 XbaI, 29 Ndel, 35 Hincll, Hpal, 39 Mlul, 47  EcoRIl,
     53 HgiCl Kpnl, 57 Ncol Styl,

61  GGAAGCTTACTCGAGGATCCGCGGATAAATAAGTAACGATCC
    CCTTCGAATGAGCTCCTAGGCGCCTATTTATTCATTGCTAGG

    63 Hindlll, 70 Aval Xhol, 75 BamHI Xho2, 79 Sac2,
```

Competitor	(U/ml)	WEHI-3B (D^{+}) cpm	WEHI-3B (D^{+}) % Inhib.	ANLL (M4) cpm	ANLL (M4) % Inhib.	ANLL (M5B) cpm	ANLL (M5B) % Inhib.
Exp. 1							
none	0	6,608	-	1,218	-	122	-
natural							
hpG-CSF:	10,000	685	90				
	2,000	1,692	74	34	97	- 376	0
	200	2,031	69				
rhpG-CSF:	10,000	0	100				
	2,000	1,185	82	202	83	0	0
	200	2,330	65				
Exp. 2							
none	0	2,910	0				
natural							
hpG-CSF:	2,000	628	78				
GM-CSF:	2,000	3,311	0				

FIG. 9